

FIGURE 1

801 MetLysHisLeuTrp
ATGAAGCATCTGTG
TACTTCGTAGACAC

851 • PhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGlnValGln
GTTCTTCCTTCTCCTAGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGC
CAAGAAGGAAGAGGATCACCGTCGAGGGTCTACCCAGGACAGGGTCCACG

901 • • LeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSer
AGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCC
TCGACGTCCTCAGCCCGGGTCTGACCACTTCGGAAGCCTCTGGGACAGG

951 LeuThrCysThrValSerGlyAlaSerIleSerSerTyrTyrTrpSerTrp
CTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAGCTG
GAGTGGACGTGACAGAGACCACGGAGGTAGTCATCAATGATGACCTCGAC

1001 • IleArgGlnProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyr
GATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATT
CTAGGCCGTCGGGGGTCCCTTCCCTGACCTACCTAACCCATATAGATAA

1051 • • SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle
ACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATA
TGTCACCCCTCGTGGTTGATGTTGGGGAGGGAGTTCTCAGCTCAGTGGTAT

1101 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuArgSerValThr
TCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGAC
AGTCATCTGTGCAGGTTCTTGGTCAAGAGGGACTTCGACTCCAGACACTG

1151 • AlaAlaAspThrAlaValTyrTyrCysAlaArgGluArgLeuGlyIleGly
CGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGAGCGACTGGGGATCG
GCGACGCCTGTGCCGGCACATAATGACACGCTCTCTCGCTGACCCCTAGC

1201 • • AspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr
GGGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC
CCCTGATGACCCCGGTTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGG

1251 LysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu
AAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTAGAGACACCTCCGA
TTCCCCGGGTAGCCAGAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCT

1301 • SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal
GAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
CTCGTGTCGGCGGGACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCC

1351 • • ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhe
TGACGGTGTCGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGACACCTTC
ACTGCCACAGCACCTTGAGTCCGCGAGACTGGTCGCCGCGACGTGTGGAAG

FIGURE 1 Continuation

1401 ProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThr
 CCAGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
 GGTGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTGCGACCACTG

 1451 •ValProSerSerAsnPheGlyThrGlnThrTyrThrCysAsnValAspHis
 CGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATC
 GCACGGGAGGTCGTTGAAGCCGTGGGTCTGGATGTGACGTTGCATCTAG

 1501 ••LysProSerAsnThrLysValAspLysThrVal
 ACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCT
 TGTTCGGGTCGTTGTGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCTGA

 1551 CAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGA
 GTCCCTCCCTCCACAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCT

 1601 CGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATC
 GCGTGGGGCCGACACGTCGGGGTCGGGTCCCGTCGTTCGGTCCGGGGTAG

 1651 TGTCTCTCAECCGGAGGCCTCTGCCCCGCCCCACTCATGCTCAGGGAGAG
 ACAGAGGAGTGGGCCTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTC

 1701 GGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCC
 CCAGAAGACCGAAAAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGG

 1751 CCTACCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGC
 GGATGGGGTCCGGGAAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACG

 1801 CAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCAAA
 GTTTTCGGTATAGGCCCTCCTGGGACGGGGACTGGATTTCGGCTGGGGTTT

 1851 GGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATC
 CCGGTTTGTACAGGTGAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAG

 1901 GluArgLysCysCysValGluCys
 CGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTGAGTG
 GCTCATTGAGGGTTAGAAGAGAGACGTCTCGCGTTTACAACACAGCTCAC

 1951 •ProProCysPro
 CCCACCGTGCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGC
 GGGTGGCAGGGTCCATTTCGGTCGGGTCCGGAGCGGAGGTGAGTTCCG

 2001 GGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGG
 CCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCC

FIGURE 1 Continuation

		AlaProProValAlaGlyPro
2051	TGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCACTGTGGCAGGAC	
	ACGACTGTGCAGGTGGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTG	
2101	••SerValPheLeuPheProProLysProLysAspThrLeuMetIleSer	
	CGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCC	
	GCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG	
2151	ArgThrProGluValThrCysValValValAspValSerHisGluAspPro	
	CGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCC	
	GCCTGGGGACTCCAGTGCACGCACCACCACCTGCACTCGGTGCTTCTGGG	
2201	•GluValGlnPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys	
	CGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA	
	GCTCCAGGTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT	
2251	••ThrLysProArgGluGluGlnPheAsnSerThrPheArgValValSer	
	AGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGC	
	TCTGTTTCGGTGCCCTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCG	
2301	ValLeuThrValValHisGlnAspTrpLeuAsnGlyLysGluTyrLysCys	
	GTCTCACC GTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTG	
	CAGGAGTGGCAACACGTGGTCTTGACCGACTTGCCGTTCCTCATGTTAC	
2351	•LysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSerLys	
	CAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAGAAAACCATCTCCA	
	GTTCCAGAGGTTGTTTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT	
2401	••ThrLys	
	AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCG	
	TTTGGTTTCCACCCTGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGC	
2451	GCTCGGCCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCC	
	CGAGCCGGGTGGGAGACGGGACCCTCACTGGCGACACGGTTGGAGACAGG	
2501	GlyGlnProArgGluProGlnValTyrThrLeuProProSerArg	
	CTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCCG	
	GATGTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCC	
2551	GluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPhe	
	GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT	
	CTCCTCTACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAA	
2601	•TyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsn	
	CTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA	
	GATGGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCT	
	••AsnTyrLysThrThrProProMetLeuAspSerAspGlySerPhePhe	

FIGURE 1 Continuation

2651 ACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC
TGTTGATGTTCTGGTGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAG

LeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnVal
2701 CTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGT
GAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCA

•PheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys
2751 CTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
GAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT

••SerLeuSerLeuSerProGlyLys
2801 AGAGCCTCTCCCTGTCTCCGGGTAAA
TCTCGGAGAGGGACAGAGGCCCATTT

FIGURE 2

901	MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrp ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCT TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGA
951	••PheProGlyAlaArgCysLysLeuAspIleGlnLeuThrGlnSerPro GGTTCCAGGTGCCAGGTGTAAGCTTGACATCCAGCTGACCCAATCTCCA CCAAGGGTCCACGGTCCACATTGCAACTGTAGGTGCGACTGGGTTAGAGGT
1001	SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCCG
1051	•SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT
1101	••AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTC TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG
1151	ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA
1201	•SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA GTGCTCGGACGTGCGACTTCTAAAACGTTGAATAATGACAGATGTGCTAT
1251	••ThrTyrProProThrPheGlyGlnGlyThrLysValGluIleLysArg ATACTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA TATGAATGGGAGGCTGCAAGCCGGTTCCTGGTTCCACCTTTAGTTTGCT
1301	ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA
1351	•LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg GAAATCTGGAAGTCTAGCGTTGTGTGCTGCTGAATAACTTCTATCCCA CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT
1401	••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn GAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAAC CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

FIGURE 2 Continuation

1451 SerGlnGluSer
TCCCAGGAGAGT
AGGGTCCTCTCA

FIGURE 3

801	<p>MetGluLeuGlyLeu</p> <p>ATGGAATTGGGGCT</p> <p>TACCTTAACCCCGA</p>
851	<p>•ArgTrpValPheLeuValAlaLeuLeuArgGlyValGlnCysGlnValGln</p> <p>CCGCTGGGTTTTCTCGTTGCTCTTTTAAGAGGTGCCAGTGTGAGGTGC</p> <p>GGCGACCCAAAAGGAGCAACGAGAAAATTCTCCACAGGTCAAGTCCACG</p>
901	<p>••LeuValGluSerGlyGlyGlyValValGlnProGlyArgSerLeuArg</p> <p>AGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA</p> <p>TCGACCACCTCAGACCCCTCCGCACCAGGTCCGACCCTCCAGGGACTCT</p>
951	<p>LeuSerCysValAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrp</p> <p>CTCTCCTGTGTAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCACTG</p> <p>GAGAGGACACATCGGAGACCTAAGTGAAGTCATCGATAACCGTACGTGAC</p>
1001	<p>•ValArgGlnAlaProGlyLysGlyLeuGluTrpValAlaValIleSerTyr</p> <p>GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCAT</p> <p>CCAGGCGGTCCGAGGTCCGTCCCGACCTCACCACCGTCAATATAGTA</p>
1051	<p>••AspGlySerAsnLysTyrTyrAlaAspSerValLysGlyArgPheThr</p> <p>ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCC</p> <p>TACTACCTTCATTATTTATGATACGTCTGAGGCACTTCCCGGCTAAGTGG</p>
1101	<p>IleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeu</p> <p>ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCT</p> <p>TAGAGGTCTCTGTTAAGGTTCTTGTGCGACATAGACGTTTACTTGTCGGA</p>
1151	<p>•ArgValGluAspThrAlaValTyrTyrCysAlaArgAspHisGlyGlyArg</p> <p>GAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGA</p> <p>CTCTCAACTCCTGTGCCGAACATAATGACACGCTCTCTAGTGCCACCCT</p>
1201	<p>••TyrValTyrAspTyrGlyMetAspValTrpGlyGlnGlyThrThrVal</p> <p>GGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC</p> <p>CCATGCAGATGCTGATGCCATACCTGCAGAAGGCGGTTCCTGGTGCCAG</p>
1251	<p>ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaPro</p> <p>ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCC</p> <p>TGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGGGGACCGCGG</p>
1301	<p>•CysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCysLeuValLys</p> <p>CTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCA</p> <p>GACGAGATCTTCGTGGAGGCTCTCGTGTGGCGGGACCCGACGGACCACT</p>
1351	<p>••AspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu</p> <p>AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCTCTG</p> <p>TCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGTCCGCGAGAC</p>

FIGURE 3 Continuation

1401 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyr
ACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTA
TGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAGTCCTGAGAT

1451 ·SerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGA
GAGGGAGTCGTGCAACCACTGGCACGGGAGGTGCTTGAAGCCGTGGGTCT

1501 ··TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLys
CCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAG
GGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTCCACCTGTTCT

1551 ThrVal
ACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCA
TGTC AACCACTCTCCGGTCGAGTCCCTCCCTCCACAGACGACCTTCGGT

1601 GGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAG
CCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGGGGTCGGGTC

1651 GGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGC
CCGTGCTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGGAGACGGGGC

1701 CCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCACCAGGCTCCA
GGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTGGTCCGAGGT

1751 GGCAGGCACAGGCTGGGTGCCCCCTACCCCAGGCCCTTCACACACAGGGGC
CCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGTGTGTCCCCG

1801 AGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCC
TCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGGCCCTCCTGGGACGGG

1851 CTGACCTAAGCCGACCCCCAAAGGCCAACTGTCCACTCCCTCAGCTCGGA
GACTGGATTCCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGAGTCGAGCCT

1901 Glu
CACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGA
GTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGAGAGACGTCT

1951 ·ArgLysCysCysValGluCysProProCysPro
GCGCAAATGTTGTGTGTCGAGTGCCACCGTGCCAGGTAAGCCAGCCCAGG
CGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCCGGTCGGGTCC

2001 CCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATC
GGAGCGGGAGGTGAGTTCCGCCCTGTCCACGGGATCTCATCGGACGTAG

2051 CAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCT
GTCCCTGTCCGGGTGACCCACGACTGTGCAGGTGAGGTAGAGAAGGA

FIGURE 3 Continuation

AlaProProValAlaGlyProSerValPheLeuPheProProLysPro
2101 CAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCAAACCC
GTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGGGGTTTGGG

LysAspThrLeuMetIleSerArgThrProGluValThrCysValValVal
2151 AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGT
TTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGCACGCACCACCA

·AspValSerHisGluAspProGluValGlnPheAsnTrpTyrValAspGly
2201 GGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACG
CCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTGC

·ValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn
2251 GCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTC AAC
CGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTCGTCAAGTTG

SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeu
2301 AGCACGTTCGGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCT
TCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGTCTTGACCGA

·AsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeuProAlaPro
2351 GAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC
CTTGCCGTTCTCATGTTACGTTCCAGAGGTGTTTCCGGAGGGTCGGG

·IleGluLysThrIleSerLysThrLys
2401 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGA
GGTAGCTCTTTTGGTAGAGGTTTTGGTTTTCCACCCTGGGCGCCCCATACT

2451 GGGCCACATGGACAGAGGCCGGCTCGGCCCAACCCTCTGCCCTGGGAGTGA
CCCCGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGGACCCTCACT

GlyGlnProArgGluProGlnVal
2501 CCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTG
GGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTTGGTGTCCAC

TyrThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeu
2551 TACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
ATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGTCCAGTCGGA

·ThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGlu
2601 GACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGG
CTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCC

·SerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMetLeu
2651 AGAGCAATGGGCAGCCGAGAACAACTACAAGACCACACCTCCCATGCTG
TCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGTGGAGGGTACGAC

AspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSer
2701 GACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAG

FIGURE 3 Continuation

CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTC

2751 ·ArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeu
CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC
GTCCACCGTCGTCCCCTTGCAAGAAGAGTACGAGGCACTACGTACTCCGAG

2801 ··HisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys
TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
ACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT

FIGURE 4

MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPhePro
901 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCC
TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGACCAAGG

••GlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSer
951 CAGGTTCCAGATGCGACATCCAGATGACCCAATCTCCATCTTCCGTGTCT
GTCCAAGGTCTACGCTGTAGGTCTACTGGGTTAGAGGTAGAAGGCACAGA

AlaSerIleGlyAspArgValSerIleThrCysArgAlaSerGlnGlyIle
1001 GCATCTATAGGAGACAGAGTCTCCATCACTTGTCGGGCGAGTCAGGGTAT
CGTAGATATCCTCTGTCTCAGAGGTAGTGAACAGCCCGCTCAGTCCATA

•SerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProThrLeu
1051 TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTACGG
ATCGTCGACCAATCGGACCATAGTCGTCTTTGGTCCCTTTCGGGGATGCG

••LeuIleTyrAlaAlaSerThrLeuGlnArgGlyValProSerArgPhe
1101 TCCTTATCTATGCTGCATCCACTTTGCAACGTGGGGTCCCATCAAGGTTC
AGGAATAGATACGACGTAGGTGAAACGTTGCACCCAGGGTAGTTCCAAG

SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln
1151 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA
TCGCCGTACCTAGACCCTGTCTAAAGTGAGAGTGGTAGTCGTCTGGACGT

•ProGluAspPheAlaThrTyrPheCysGlnGlnAlaAsnSerPheProPhe
1201 GCCTGAAGATTTTGCAACTTACTTTTGCAACAGGCTAACAGTTTCCCAT
CGGACTTCTAAACGTTGAATGAAAACAGTTGTCCGATTGTCAAAGGGTA

••ThrPheGlyProGlyThrLysValAspIleLysArgThrValAlaAla
1251 TCACTTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCA
AGTGAAAGCCGGGACCCTGGTTTCACCTATAGTTTGCTTGACACCGACGT

ProSerValPheIlePheProProSerAspGluGlnLeuLysSerGlyThr
1301 CCATCTGTCTTCATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGAAC
GGTAGACAGAAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTG

•AlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysVal
1351 TGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
ACGATCGCAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTC

••GlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSer
1401 TACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGT
ATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATGAGGGTCCTCTCA

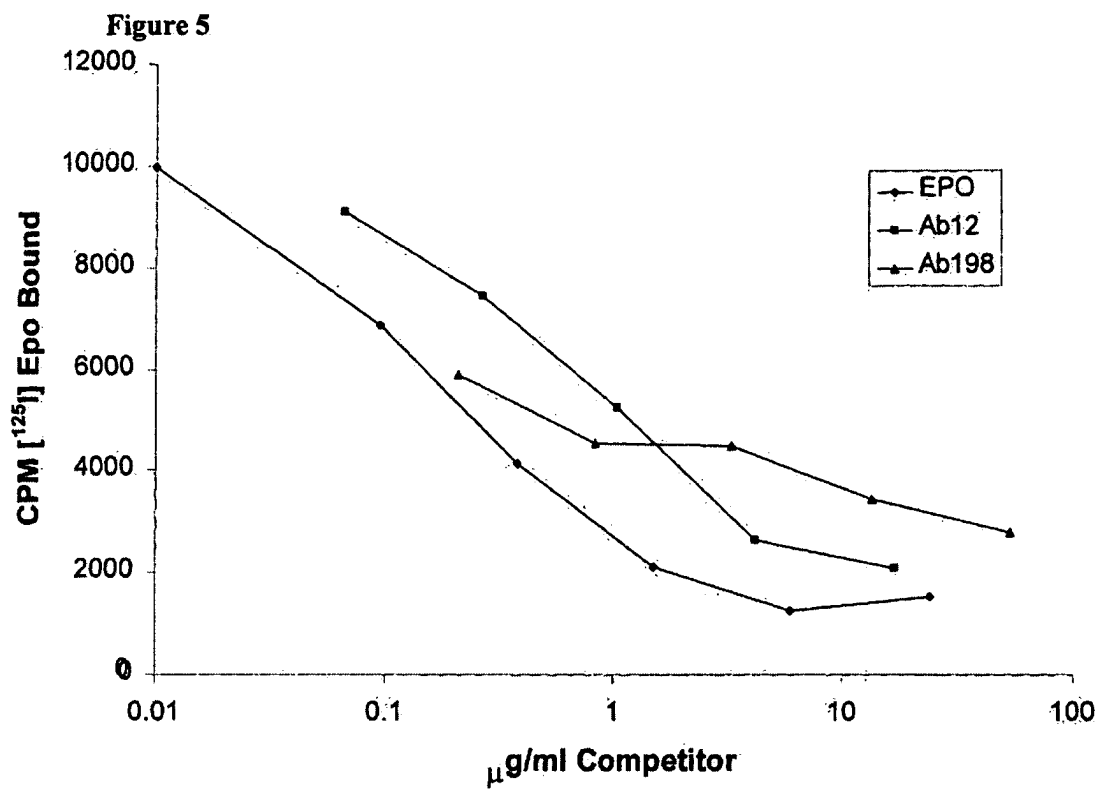
ValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeu
1451 GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCT
CAGTGTCTCGTCCTGTCGTTCTGTCGTGGATGTCGGAGTCGTCGTGGGA

FIGURE 4 Continuation

•ThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluVal
1501 GACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG
CTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACGCTTC

••ThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGly
1551 TCACCCATCAGGGECTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGA
AGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCGAAGTTGTCCCT

GluCys
1601 GAGTGT
CTCACA



Erythropoietic Activity of Ab Candidates on F36e Human Erythroleukemic Cell Line

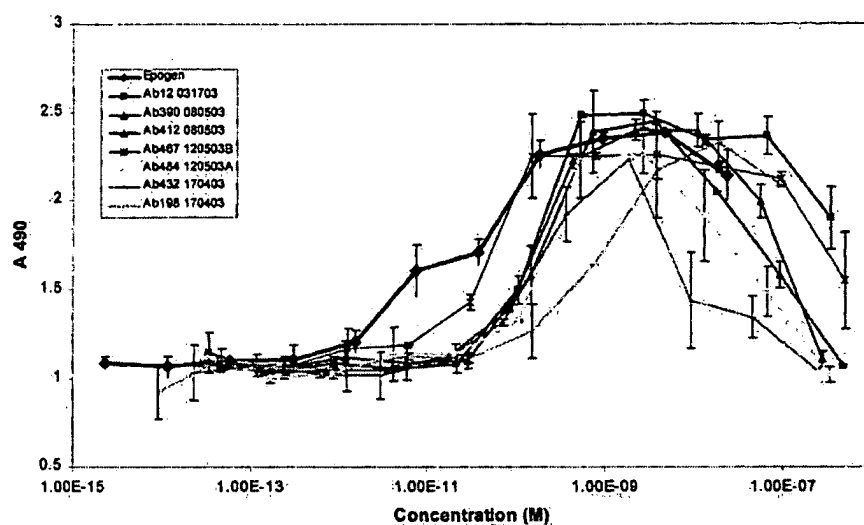


FIGURE 6

Figure 7

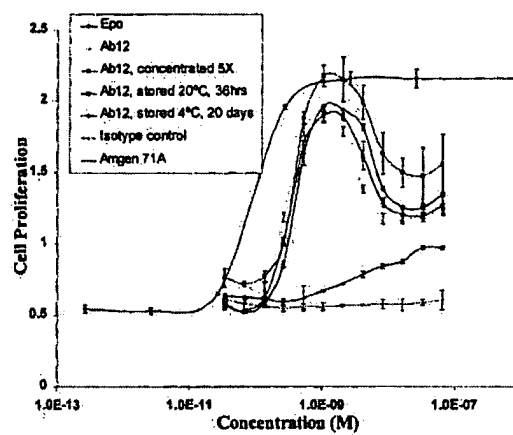
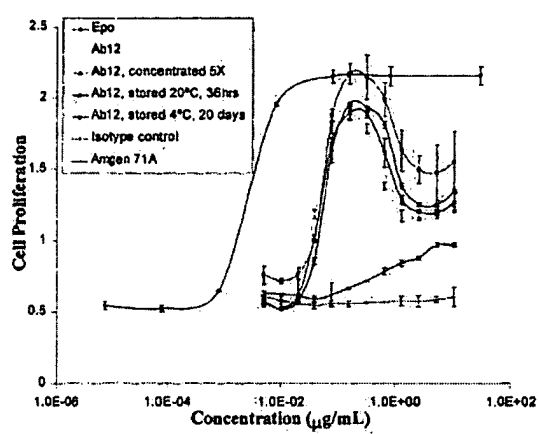
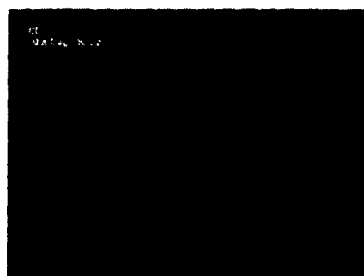


Figure 8

No Epo Control

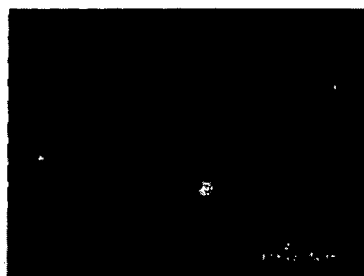


3 U/ml Epo



150 colonies / dish

500 ng/ml Ab12



48 colonies / dish

Figure 9

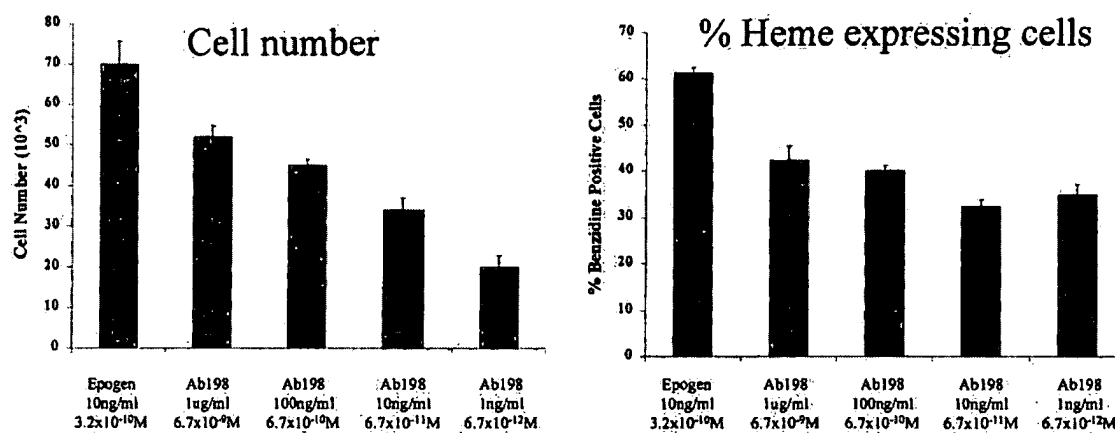
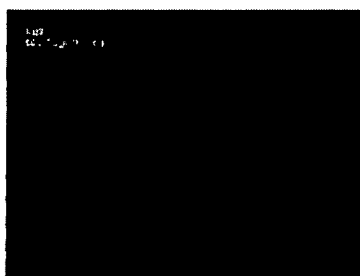
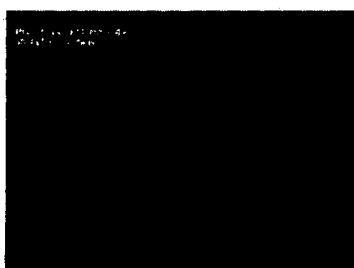


Figure 10

No Epo Control



3 U/ml Epo



3200 ng/ml Ab12

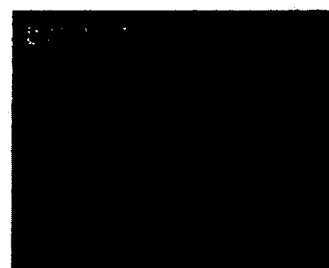


Figure 11

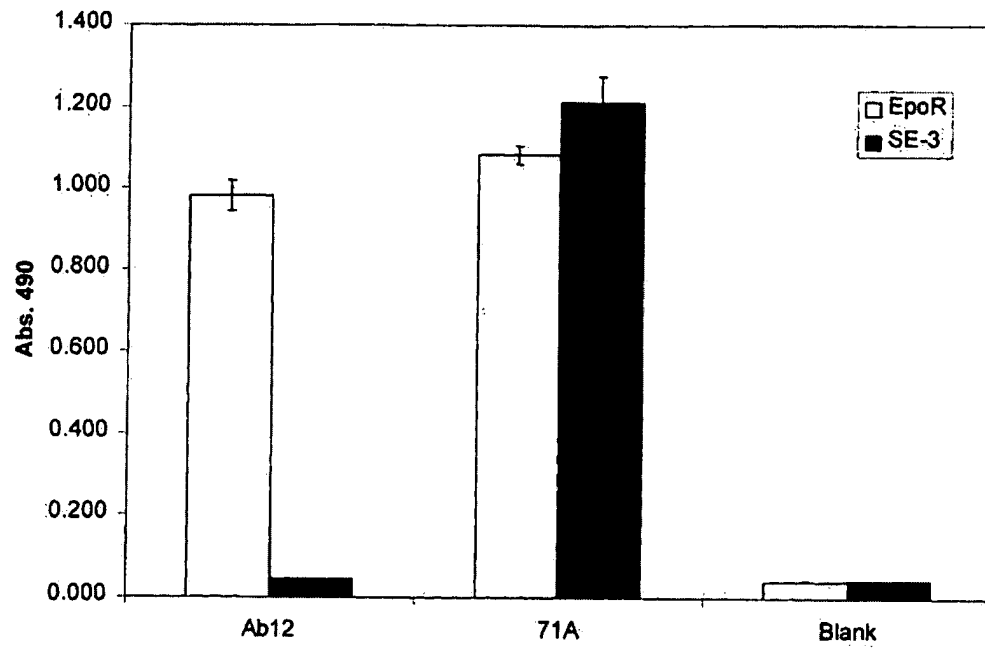


Figure 12

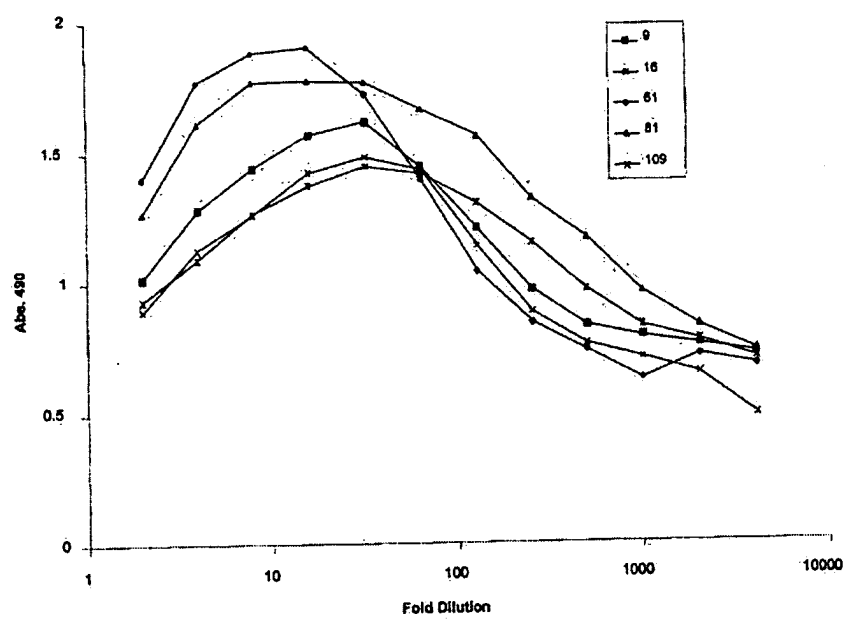


Figure 13

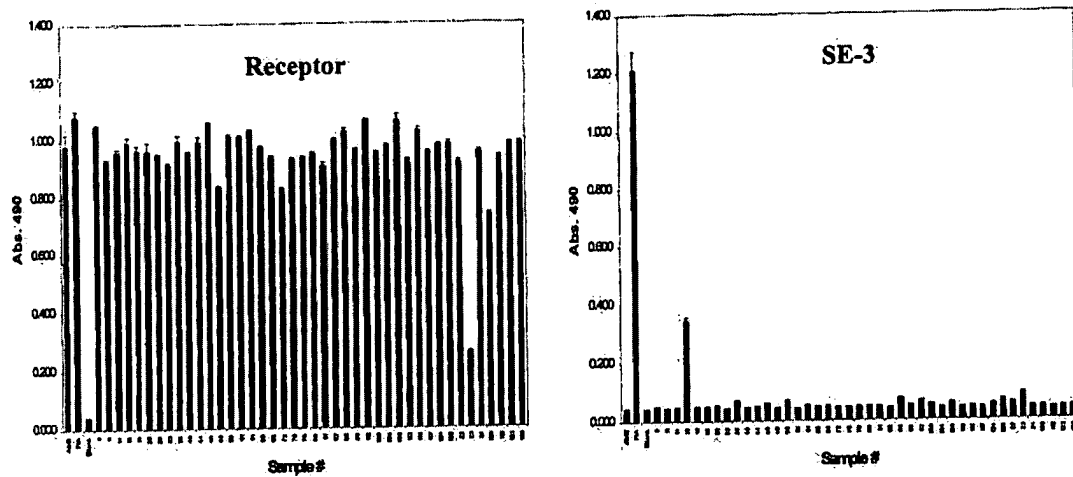


Figure 14

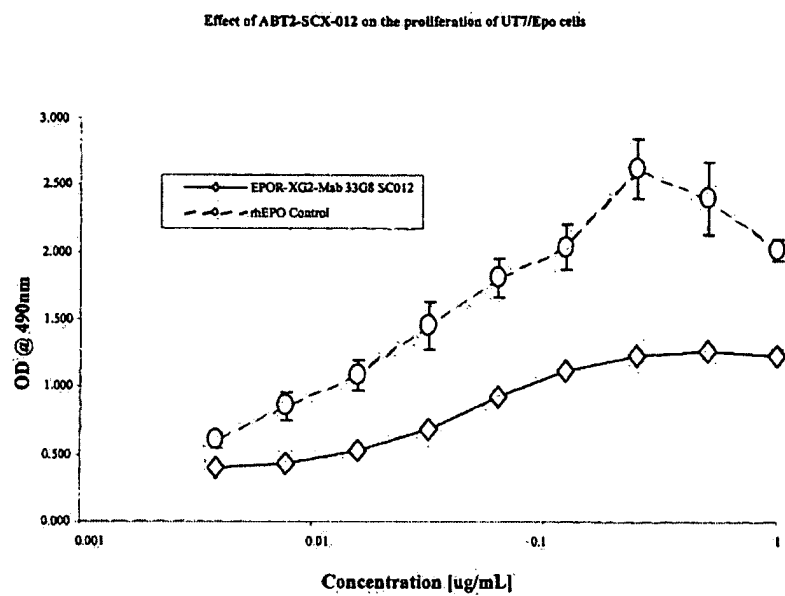


Figure 15

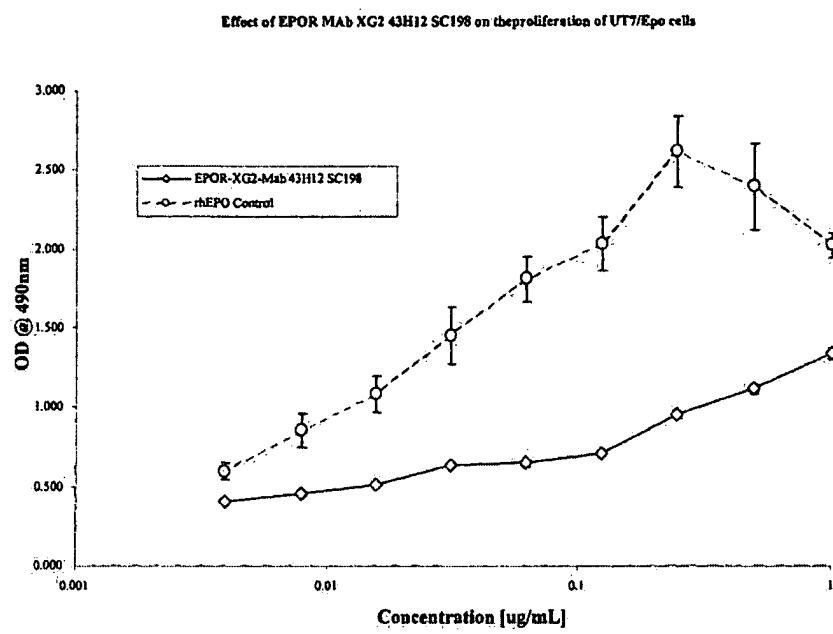


Figure 16

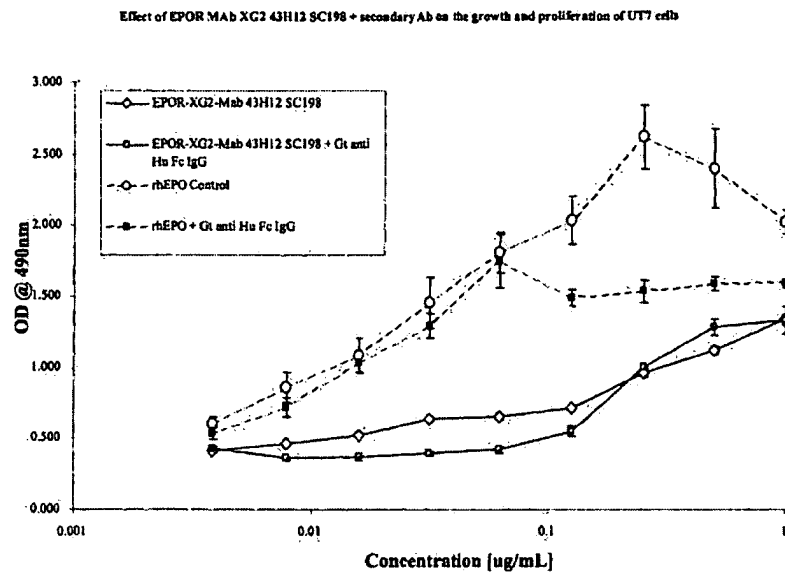


Figure 17

Effect of ABT2-SCX-012 + secondary Ab on the proliferation of UT7/Epo cells

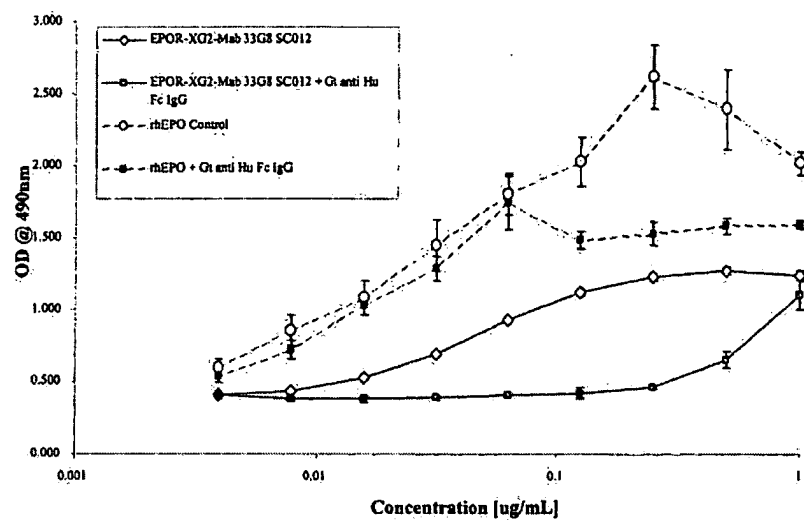


FIGURE 18

A-- ABT2-SCX-003 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-003 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-003 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGTCTGG
TATCAGCAGAAACCAGGGAAAGCCCTGCGCTCCTAATCTATGCTGCATCCA
GTTTGCAGCGTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGA
CTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTTT
GTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC3'

D-- ABT2-SCX-003 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGD RVSITCRASQGISSWLVWYQQKPGKAPALLIYAASSLQ
RGVPSRFSGSGSGTDFLTISLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 19

A-- ABT2-SCX-012 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTAT
TACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGAGCGACTGGGGATCGGGGAC
TACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-012 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGASISSYYWSWIRQPPGKGLEWIGYIYYSGS
TNYNPSLKSRTISVDTSKNQFSLKLSVTAADTAVYYCARERLIGIDYWGQGT
LVTVSS

C-- ABT2-SCX-012 Nucleotide sequence of light chain variable region:

5'GACATCCAGCTGACCCAATCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
AATTCACCTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTAC
TGTCTACAGCATAATACTTACCCTCCGACGTTCCGGCCAAGGGACCAAGGTGG
AAATCAAAC3'

D-- ABT2-SCX-012 Amino acid sequence of light chain variable region:

DIQLTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPPTFGGQGTKVEIK

FIGURE 20

A-- ABT2-SCX-022 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGTAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAECGTCT
CCTCAG3'

B-- ABT2-SCX-022 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVVVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWVGQGTITVTVSS

C-- ABT2-SCX-022 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCCGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCAC TTTCCGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-022 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGD RVSITCRASQGISSWLAWYQQKPGKAP TLLIYAASSLQ
RGVPSRFSGSGSGTDFLTITISLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 21

A-- ABT2-SCX-054 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAAATATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTTTATG
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCC
ATCTCCAGAGACAATTCCAAGAACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTCCGTACTACTTTGA
CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-054 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSKYGMHWVRQAPGKGLEWVAVLW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGPYFDY
WGQGLVTVSS

C-- ABT2-SCX-054 Nucleotide sequence of light chain variable region:

5'GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAA
GAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGC
CTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCA
TCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGA
CAGACTTCACTGTCACCATCAGCAGACTGGAACCTGAAGATTTGCAGTGTAT
TACTGTCAGCAGTATGGTAGTTCACCGTGGACGTTCCGCCAAGGGACCAAGG
TGGAATCAAAC3'

D-- ABT2-SCX-054 Amino acid sequence of light chain variable region:

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASSRA
TGIPDRFSGSGSGTDFTVITISRLPEDFAVYYCQYQGSSPWTFGQGTKVEIK

FIGURE 22

A-- ABT2-SCX-060 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-060 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-060 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCCGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-060 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLA WYQQKPGKAP TLLIYAASSLQ
RGVPSRFSGSGSGTDFLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 23

A-- ABT2-SCX-102 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-102 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-102 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-102 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPKRLIYAASSLQ
RGVPSRFSGSGSDFTLTISLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 24

A-- ABT2-SCX-135 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-135 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWVGQTTVTVSS

C-- ABT2-SCX-135 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTACATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCATTTTCGGCCCTGGGACCAAAGTGA
TGTC AAAC3'

D-- ABT2-SCX-135 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSTSVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFLTINSLQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 25

A-- ABT2-SCX-145 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-145 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-145 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCATTTGGGCCCTGGGACCAAAGTGGA
TGTC AAAC3'

D-- ABT2-SCX-145 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGD RVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFLTINS LQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 26

A-- ABT2-SCX-198 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGTAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-198 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWVGQGTITVTVSS

C-- ABT2-SCX-198 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTATAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTTATCTATGCTGCATCC
ACTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTC AACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-198 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASIGDRVSITCRASQGISSWLAWYQQKPGKAPTLLIYAASLQR
GVPSRFSGSGSGTDFLTISLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 27

A-- ABT2-SCX-254 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGG
TTTGATGGAAATAATAAATTCTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTCGAGGACACGGCTGTGTATTACTGTGCGCGAGGCGGGAGCTACTGGGAC
TACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-254 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWF
DGNKIFYADSVKGRFTISRDN SKNTLYQMNSLRVEDTAVYYCARGGSYWDY
WGQGTLVTVSS

C-- ABT2-SCX-254 Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACCCAGACTCCACTCTTCTCATTTGTCATGATTGGACAGC
CGGCCTCCATCTCCTGCAGGTCTAGGCAAAGCCTCGTACACAGTGATGGAAA
CACCTACTTGAATTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCTA
ATTTATAAGACTTCTAACC GGTTCTCTGGGGTCCCAGATAGATT CAGTGGCAG
TGGGGCAGGGACAGATTTCACTGAAAATCAGCAGGGTGGAAAGCTGAGGA
TGTCGGGGTTTATTACTGTATGCAAGCTACACAATTTCTATCACGTTCCGCC
AAGGGACACGACTGGAGATTAAA3'

D-- ABT2-SCX-254 Amino acid sequence of light chain variable region:

DIVMTQTPLFSFVMIGQPASISCRSRQSLVHSDGNTYLNWLQQRPGQPPRLIYKT
SNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPITFGQGTREI
K

FIGURE 28

A-- ABT2-SCX-267 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTCCGAAAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-267 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCAKD HGGRYV
YDYGMDVWGQGTTVTVSS

C-- ABT2-SCX-267 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCTGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCCTCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TGTCAAAC3'

D-- ABT2-SCX-267 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGD RVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFTLTINS LQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 29

Single Cell	V Heavy/D/J	FR1	CDR1	FR2	CDR2
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGQH	MVRQAPGKLEWVA	VISYDGSNKYYADSVKG
3	VH3-30 (V3-30)/D4-23/JH6b	-----V-----	-----	-----V-----	-----
22		-----V-----	-----	-----	-----
60		-----V-----	-----	-----	-----
102		-----V-----	-----	-----	-----
135		-----V-----	-----	-----	-----
145		-----V-----	-----	-----	-----
198		-----V-----	-----	-----	-----
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGQH	MVRQAPGKLEWVA	VISYDGSNKYYADSVKG
267	VH3-30.5 (DP-49)/D4-23/JH6b	-----	-----	-----	-----
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGQH	MVRQAPGKLEWVA	VISYDGSNKYYADSVKG
54	VH3-33 (DP-50)/DIR3/JH4b	-----K-----	-----	-----	-----L-----
254	VH3-33 (DP-50)/D21-10rc/JH4b	-----	-----	-----	-----F--N--F-----
-	Germline	QVQLQESGPGLVKPKSETLSLTCTVS	GGSISSYYWS	MIRQPPGKLEWIG	YIYYSGSTNYNPSLKS
12	VH4-59 (DP-71)/DIR4rc/JH4a	-----A-----	-----	-----	-----

Single Cell	V Heavy/D/J	FR3	CDR3	FR4
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	DHGGRVYDYGHMV	WGQGTITVTVSS
3	VH3-30 (V3-30)/D4-23/JH6b	-----V-----	-----	-----
22		-----V-----	-----	-----
60		-----V-----	-----	-----
102		-----V-----	-----	-----
135		-----V-----	-----	-----
145		-----V-----	-----	-----
198		-----V-----	-----	-----
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	-----	WGQGTITVTVSS
267	VH3-30.5 (DP-49)/D4-23/JH6b	-----V-----	-----	-----
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	-----	WGQGTITVTVSS
54	VH3-33 (DP-50)/DIR3/JH4b	-----	GPYYFDY	-----
254	VH3-33 (DP-50)/D21-10rc/JH4b	-----V-----	GGSYWDY	-----
-	Germline	RVTISVDTSKQFSLKLSVTAADTAVYYCAR	-----	WGQGTITVTVSS
12	VH4-59 (DP-71)/DIR4rc/JH4a	-----R-----	ERLGIGDY	-----

Figure 30

Single Cell	V Kappa/J	TR1	CDR1	TR4	CDR2
-	XXXXXXXXXXXX	RIVLDQSPGTLISLGERATLGC	RASQSVSSSYLA	WYQDQFGQAPRLITY	QASSRAT
54	VHII (A27)/Jk1	-----	-----	-----	-----
-	XXXXXXXXXXXX	DIQMDSFSSVSASVGRVTTC	RASQISSEILA	WYQDQFGHAPRLITY	AASSIQS
3	VH1 (L5)/Jk3	-----S-----	-----V-----	-----R-----	-----R-----
22		-----S-----	-----T-----	-----R-----	-----R-----
60		-----S-----	-----T-----	-----R-----	-----R-----
102		-----S-----	-----R-----	-----R-----	-----R-----
135		-----T-----S-----	-----G-----	-----Q--T-----	-----R-----
145		-----S-----	-----G-----	-----Q--T-----	-----R-----
198		-----X-----S-----	-----T-----	-----T-----	-----T--R-----
267		-----S-----	-----G-----	-----Q--T-----	-----R-----
-	XXXXXXXXXXXX	DIQMDSFSSVSASVGRVTTC	RASQIRMDLA	WYQDQFGHAPRLITY	AASSIQS
12	VH1 (A30)/Jk1	-----L-----	-----	-----	-----
-	XXXXXXXXXXXX	DIVMDVTLAGFTLQGFATISC	RSSQLVHSDGTYLS	WLOQRFGQFPRLITY	KISMRFS
254	VHII (A23)/Jk3	-----T--P--MI-----	--R-----N-----	-----	-----T-----

Single Cell	V Kappa/J	TR1	CDR1	J
-	XXXXXXXXXXXX	QIFDRFSSGSGVDFTLTISLQPEDFAVYC	QQYGSFPWT	FGQGVKLEIK
54	VHII (A27)/Jk1	-----V-----	-----	-----
-	XXXXXXXXXXXX	GVPERFSGSGSGVDFTLTISLQPEDFATYC	QQANSFPTT	FQFGKVDIK
3	VH1 (L5)/Jk3	-----F-----	-----	-----
22		-----F-----	-----	-----
60		-----F-----	-----	-----
102		-----F-----	-----	-----
135		-----N-----F-----	-----	-----V-----
145		-----N-----F-----	-----	-----V-----
198		-----F-----	-----	-----
267		-----N-----F-----	-----	-----
-	XXXXXXXXXXXX	GVPERFSGSGSGVDFTLTISLQPEDFATYC	LOHSEYPTT	FGQGVKLEIK
12	VH1 (A30)/Jk1	-----T-----	-----	-----
-	XXXXXXXXXXXX	GVPERFSGSGSGVDFTLTISLQPEDFATYC	MQATQFTTT	FGQGVKLEIK
254	VHII (A23)/Jk3	-----	-----	-----

Comparison of Erythropoietic Activity of Gamma 1 Ab-12 versus Gamma 2 Ab-12 on F36e Human Erythroleukemic Cell Line

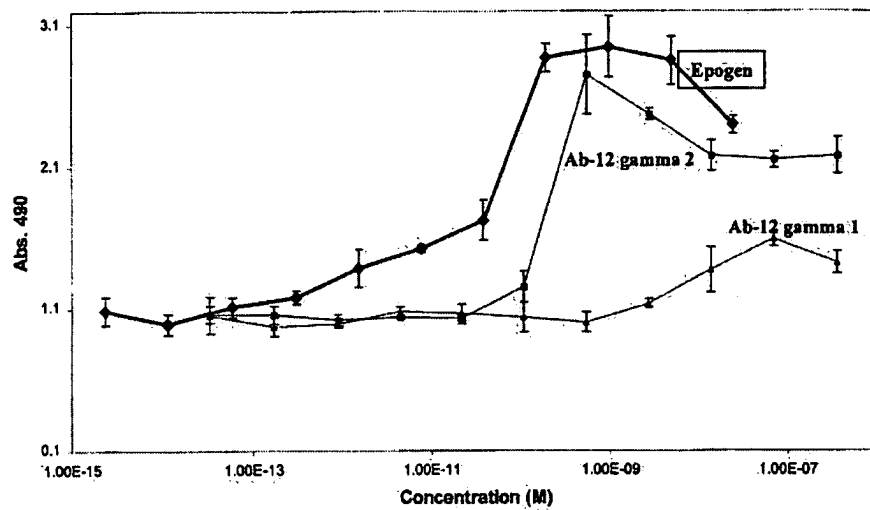
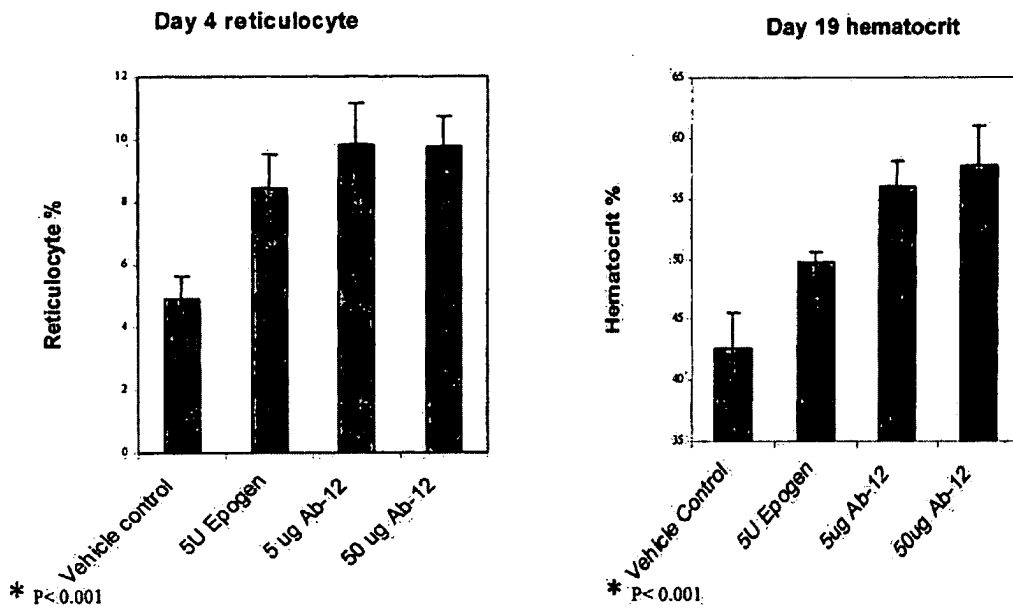


FIGURE 31

FIGURE 32

Ab-12 Increases Reticulocyte Count and Hematocrit in Transgenic Mice



Day 19 Hematocrit in Transgenic Mice Following Weekly Dosing with Ab-12 or Aranesp

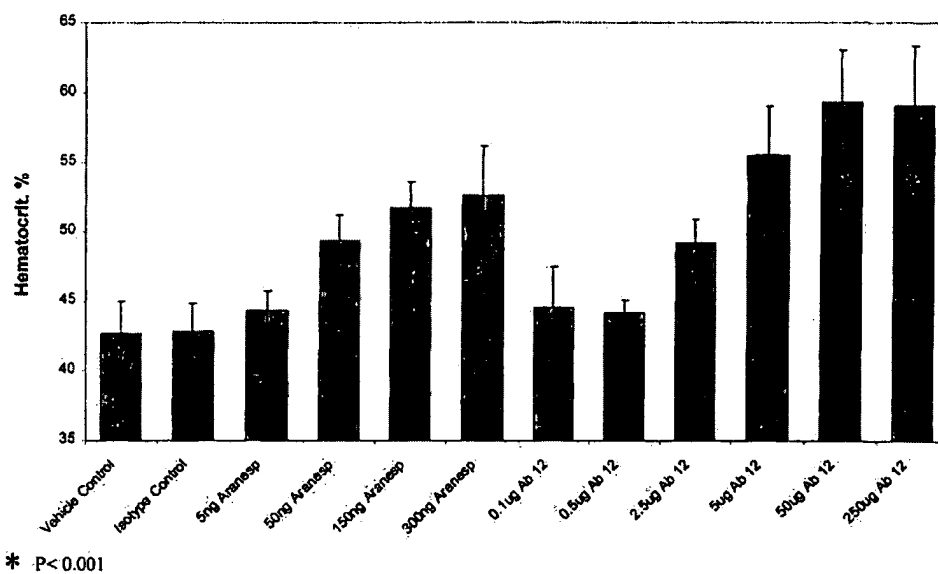


FIGURE 33

Day 19 Hematocrit in Transgenic Mice Comparing Single vs. Weekly Dosing with Ab-12 or Aranesp

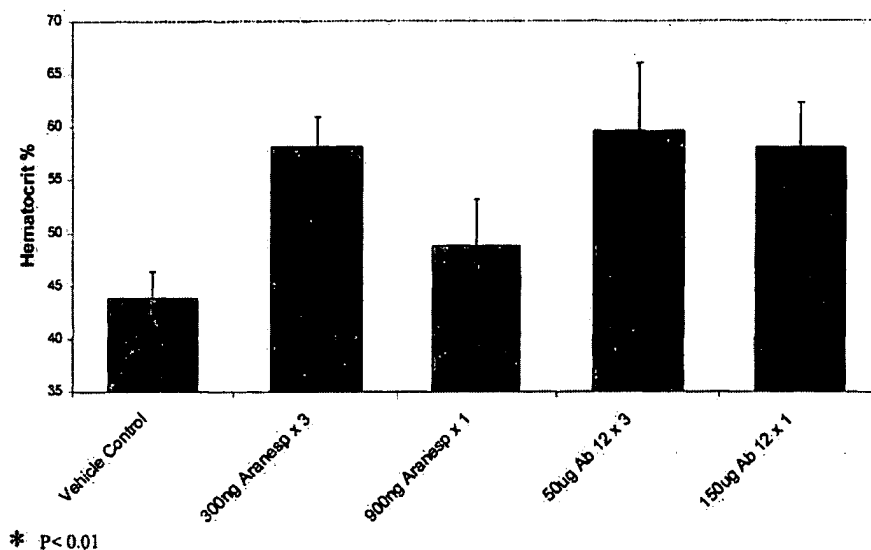


FIGURE 34

FIGURE 35

A. Ab390 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAATTACTACTGG
AGCTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTC
TCTTACAGTGGGAGTACGTACTACAACCCCTCCCTCAAGGGTCGAGTCACC
ATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTG
ACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGAAAACTGGGGATT
GGAGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA3'

B. Ab390 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGASISNYYSWIRQPPGKLEWIGYVSYS
GS
TYYNPSLKGRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAREKLGIGDYWGQGLV
TVSS

C. Ab390 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAAAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTATCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3'

D. Ab390 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFQGQTKLEIK

FIGURE 36

A. Ab412 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGCAGTGGTGCTTACTA
CTGGAGTTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAAGAGTGAGACCTCCTACTACAACCCGTCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTATTGTGCGAGAGATAAACTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3'

B. Ab412 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSQTLSTCTVSGASISSGAYYWSWIRQHPGKGLEWIGY
IYKSETSYNPSLKSRLTSLVDTSKNQFSLNLSVTAADTAVYYCARDKLG
ADYWGQGTLVTVSS

C. Ab412 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGACATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCC
AATTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCCTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTTGCGCGGAGGGACCAAGGTG
GAAATCAAAC3'

D. Ab412 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPKAPKRLIYAAS
NLQSGVPSRFSGSGSTEFTLTISLQPEDFATYYCLOHNSYPPTFGGGTKV
EIK

FIGURE 37

A. Ab432 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGTCTCCATCAGTAATTACTACTGGAG
CTGGATCCGGCAGTCCCCAGGGAAGGGACTGGAGTGGATTGGATATATCTAT
TACAGTGGGAGTCCCTATTACAACCCCTCCCTCAAGAGTCGAGTCACTATAT
CTGCAGACACGTCCAAGAACCAATTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCATTTATTACTGTGCGAGAGAAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG3'

B. Ab432 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGVSI SNYYWSWIRQSPGKGLEWIGYIY
YSGSPYYNPSLKS RVTISADTSKNQFSLKLSVTAADTAIYYCAREKLGIGD
YWGQGLVTVSS

C. Ab430 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCTCCC ACTTTCGGCCCTGGGACCAAGGTG
GATATCAAAC3'

D. Ab430 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFS GSGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGPGTKV
DIK

FIGURE 38

A. Ab467 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTCGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTCTCT
TACAGTGGGAGCACCTACTACAACCCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAG3'

B. Ab467 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSSETLSLTCTVSGGSISRYYSWIRQPPGKGLEWIGYVS
YSGSTYYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAVYYCARDKLGIGD
YWGQGLTVTVSS

C. Ab467 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCGGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAG
AATTCCTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3'

D. Ab467 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVITICRASQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPCSFQGQTKL
EIK

FIGURE 39

A. Ab484 nucleotide sequence of heavy chain variable region:

5' CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTTACAGACCC
TGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGTCTACTA
CTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAACAGTAAGACCTCCTATTATAATCCGTCCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAATTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B. Ab484 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPLQTLSTCTVSGGSISSGVYYWSWIRQHPGKGLEWIGY
IYNSKTSYYNPSLKSRLTSLVDTSKNQFSLNLISVTAADTAVYYCARDKLG
ADYWGQGLTVTVSS

C. Ab484 nucleotide sequence of light chain variable region:

5' GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGACAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAG
AATTCCTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTCGGCGGAGGGACCAAGGTG
GAGATCAAAC3'

D. Ab484 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGGGTKV
EIK

1212	Seq. 1212	Chain 10	V. Recy. C.1	1212	Seq. 1212
-	-	-	-	QVGLVSGGGYVVKPSLRLSCAAS	GYTFSSTQHL
43812	190	14325.3	VW3-30/D4-23/JH4	-----V--	WVRGAPGAGLEWVA
-	-	-	-	QVGLVSGGGYVVKPSLRLSCAAS	-----V--
3308	12	13308.1	VW4-59/DIR4C/JH4	QVGLVSGGGYVVKPSLRLSCAAS	WVRGAPGAGLEWIG
-	-	-	-	-----A--	-----A--
230A4	412	54995.1	V4-31/DIR4C/JH4	QVGLVSGGGYVVKPSLRLSCAAS	WVRGAPGAGLEWIG
-	-	-	-	-----G--	-----A--
208A12	404	57130.1	V4-30.1/DIR4C/JH4	QVGLVSGGGYVVKPSLRLSCAAS	WVRGAPGAGLEWIG
-	-	-	-	-----L--	-----V--
259C12	467	56979.2	V4-59/D1-27/JH4	QVGLVSGGGYVVKPSLRLSCAAS	WVRGAPGAGLEWIG
234D12	380	57141.2	VW4-59/D1-27/JH4B	-----A--	-----N--
223W2	432	57354.11	VW4-59/D1-27/JH4B	-----V--	-----S--

1212	Seq. 1212	Chain 10	V. Recy. C.1	1212	Seq. 1212
190	VISTGGSHYIAQSVKQ	RFTISPDWIKQTLVOMKSLRAQDAVITYCAK	OWGDAVYDYQNDV	WQGTIVTVSS	-----
-	-----	-----R	-----	-----	-----
16	YIYEGSYINPFLAS	RVTISVDTSKQFSLKLSRTAADTAIVTCAR	ERLGLGDY	WQGTIVTVSS	-----
-	-----	-----R	-----	-----	-----
412	YIYEGSYINPFLAS	PVTISVDTSKQFSLKLSRTAADTAIVTCAR	DKLGLADY	WQGTIVTVSS	-----
-	-----K-ETS-----	-----L-L-----	-----	-----	-----
404	YIYEGSYINPFLAS	RVTISVDTSKQFSLKLSRTAADTAIVTCAR	DKLGLADY	WQGTIVTVSS	-----
-	-----H-KTS-----	-----L-L-----	-----	-----	-----
467	YIYEGSYINPFLAS	RVTISVDTSKQFSLKLSRTAADTAIVTCAR	DKLGLGDY	WQGTIVTVSS	-----
-	-----V-E-----	-----R-----	-----	-----	-----
380	YIYEGSYINPFLAS	RVTISVDTSKQFSLKLSRTAADTAIVTCAR	DKLGLGDY	WQGTIVTVSS	-----
430	YIYEGSYINPFLAS	RVTISVDTSKQFSLKLSRTAADTAIVTCAR	DKLGLGDY	WQGTIVTVSS	-----

Figure 40

Ref	Accession	Protein	Enzyme	Substrate	Product	Enzyme	Substrate	Product
43812	158	24325.3	15/263	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
3108	12	13308.1	A38/263	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
23382	430	54494.3	A38/263	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
23384	412	54732.2	A38(V61)/264	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
208A12	484	57094.1	A38(V61)/264	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
259C12	467	56556.1	A38(V61)/262	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		
234D12	390	56829.3	A38(V61)/262	D1QNTQSPRELAASVQDEVTTC	RAAQIIRNLA	WTQKPGKAFELIY		

Ref	Accession	Protein	Enzyme	Substrate	Product
198	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	Q0ANSFPT	PGQTTVDIR	
12	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	
430	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	
412	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	
484	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	
464	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	
390	AASLQ9	GVPSFDSGSGTFTLTISLQPEDFATTC	LQMSYPT	PGQTTVIR	

Figure 41

FIGURE 42

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAGCATCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTCGTAGACACCAAGAAGGAAGAGGACCACC

51 ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCAGATGGGTCTGTCCAGGTGCAGCTGCAGGAGTCGGGCCCCA
GTCGAGGGTCTACCCAGGACAGGGTECACGTGGACGTCCTCAGCCCGGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·AlaSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnProProGlyLys
TGCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGCCCCAGGGA
ACGGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTCGGGGGTCCCT

201 ··GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGTACGTACTAC
TCCCTGACCTCACCTAACCATAACAGAGAATGTCACCCTCATGCATGATG

251 AsnProSerLeuLysGlyArgValThrMetSerValAspThrSerLysAsn
AACCCTCCCTCAAGGGTCGAGTCACCATGTCAGTAGACACGTCCAAGAA
TTGGGGAGGGAGTTCACAGCTCAGTGGTACAGTCATCTGTGCAGGTTCTT

301 ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGCACA

351 ··TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTTTTGGACCCCTAACCTCTGATGACCCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCTGGGTAGCCAGAAGGG

451 ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTCTGTTGGAGGCTCTCGTGTGCGCGGGACCCGA

501 ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCA
CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
GGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCTACAGTCCTC
CCGCGAGACTGGTCGCCGACGTGTGGAAGGGTCGACAGGATGTCAGGAG

FIGURE 42 Continuation

601 ·GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

651 ··ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTC

701 ValAspLysThrVal
GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCACAGACG

751 TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCGGGCTGTGCAGCC
ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
GGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCGCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCAC
AGACGGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAAGACCGAAAAAGGTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCCTACCCAGGCCCTTCACA
GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTGGGTATAGGCCCTCC

1001 ACCCTGCECCTGACCTAAGCCGACCCCAAAGGCCAACTGTCCACTCCCT
TGGGACGGGGACTGGATTCCGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCAGATCCGAGTAACTCCCAATCTTCT
GTCGAGCCTGTGGAAGAGAGGAGGTCTAGGCTCATTGAGGGTTAGAAGA

1101 GluArgLysCysCysValGluCysProProCysPro
CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCAGGTAAGC
GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCTG

1151 CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
GTCGGGTCCGGAGCGGGAGGTGAGTTCGGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

1251 AlaProProValAlaGlyProSerValPheLeuPhePro
TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCTCTTCCCC
AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys·

FIGURE 42 Continuation

1301 CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
GGTTTTGGGTTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

•ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr•
1351 CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

••ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
TGCACCTGCCGCACCTECACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln•
1451 CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
GTCAAGTTGTCTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGT

•AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu•
1501 GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
CCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGTTTCCGG

••ProAlaProIleGluLysThrIleSerLysThrLys
1551 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCCTGGGCG

1601 GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCCCTCTGCCC
CCCCATACTCCCGGTGTACCTGTCTCGGGCCGAGCCGGGTGGGAGACGGG

GlyGlnProArgGlu
1651 TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCGAGAA
ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln•
1701 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

•ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal•
1751 GGTACGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG
CCAGTCGGACTGGACGGACCAAGTTCCGAAGATGGGGTCGCTGTAGCGGC

••GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACACCT
ACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal•
1851 CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCA

•AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis•

FIGURE 42 Continuation

1901 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

••GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro

1951 ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

GlyLys

2001 GGTAAG
CCATTT

FIGURE 43

1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGCTCCCCGCTCAGCTCCTGGGGCTCCTGC
TACTCCGAGGGGCGAGTCGAGGACCCCGAGGACG

51 ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

151 ·SerGlnGlyIleLysAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGGCATTAAAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
TTCAGTCCCGTAATTTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAAT
GGTAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
GTCGTCCGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ··SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
ATAGTTATCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
TATCAATAGGCACGTCAAAACCGGTCCCTGGTTTCGACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAAGTCTAGCGTTGEGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCTGTTCTGTCTGGATGTCGGA

FIGURE 43 Continuation

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGGCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 44

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
 ATGAAACATCTGTGGTCTTCCTCCTGCTGGTGG
 TACTTTGTAGACACCAAGAAGGAGGACGACCACC

51 ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
 CAGCTCCCAGATGGGTCTGTCCAGGTGCAGCTGCAGGAGTCGGGCCCA
 GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCCGGT

101 GlyLeuValLysProSerGlnThrLeuSerLeuThrCysThrValSerGly
 GGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
 CCTGACCACTTCGGAAGTGTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·AlaSerIleSerSerGlyAlaTyrTyrTrpSerTrpIleArgGlnHisPro
 TGCCTCCATCAGCAGTGGTGCTTACTACTGGAGTTGGATCCGCCAGCACC
 ACGGAGGTAGTCGTCACACGAATGATGACCTCAACCTAGGCGGTCTGTGG

201 ··GlyLysGlyLeuGluTrpIleGlyTyrIleTyrLysSerGluThrSer
 CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAAGAGTGAGACCTCC
 GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTCTCACTCTGGAGG

251 TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
 TACTAGAACCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
 ATGATGTTGGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

301 ·LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
 TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
 ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

351 ··ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
 CCGTGTATTATTGTGCGAGAGATAAACTGGGGATCGCGGACTACTGGGGC
 GGCACATAATAACACGCTCTCTATTTGACCCCTAGCGCCTGATGACCCCG

401 GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
 CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
 GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCA

451 ·PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
 CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCC
 GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGGCGGG

501 ··GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
 TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGG
 ACCCGACGGACCACTTCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

551 AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
 AACTCAGGCGCTCTGACCAGCGGCGTGACACCTTCCCAGCTGTCTACA
 TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT

FIGURE 44 Continuation

601 ·SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
CAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGT

651 ··PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
ACTTCGGCACCCAGACCTACACGTGCAACGTAGATCACAAGCCCAGCAAC
TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTG

701 ThrLysValAspLysThrVal
ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
TGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751 GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT
CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801 GCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCG
CGTCGGGGTTCGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGC

851 GAGGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
CTCCGGAGACGGGCGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAA

901 TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCCAGGCCC
AAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951 TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
AAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGG

1001 GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
CCCTCCTGGGACGGGGACTGGATTCCGGCTGGGGTTTCGGGTTTGACAGGT

1051 CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

1101 GluArgLysCysCysValGluCysProProCysPro
TCTTCTCTCTGCAGAGCGCAAATGTTGTGTGCGAGTGCCACCGTGCCAG
AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTC

1151 GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
CATTCCGGTCGGGTCCGGAGCGGGAGGTCGAGTTCCGECCTGTCCACGGGA

1201 AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

1251 AlaProProValAlaGlyProSerValPheLeu
CCTCCATCTCTTCTCAGCACCCACCTGTGGCAGGACCGTCAGTCTTCTC
GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal

FIGURE 44 Continuation

1301 TTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
AAGGGGGGTTTGGGTTCCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

•ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
1351 CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCGAGGTCCAGTTCA
GTGCACGCACCACCACTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGT

••TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
1401 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
TGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCC

GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
1451 GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT
CTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

•HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
1501 GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
CGTGGTCCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGT

••GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
1551 AAGGCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCC

1601 ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCCACCCT
TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

GlyGlnPro
1651 CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGG

ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
1701 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAA
GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGTT

•AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
1751 GAACCAGGTCAAGCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACA
CTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATGGGGTCGCTGT

••AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
1801 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
AGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG

ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
1851 ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCT
TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTGCTTCGA

•ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
1901 CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG

FIGURE 44 Continuation

GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

1951 ··MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
TGATGCATGAGGGTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

2001 SerProGlyLys
TCTCCGGGTAAA
AGAGGCCCATTT

FIGURE 45

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
TACTCCCAGGGGCGAGTCGAGGAACCCGAGGACG

51 ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGCGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCGCGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

151 ·SerGlnAspIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGACATTAGAAATGATTTAGGCTGGTATGAGCAGAAACCAGGGA
TTCAGTCCTGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ··AlaProLysArgLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAATTTGCAAAGTGGGGTC
TTCCGGGATTTCGCGGACTAGATACGACGTAGGTAAACGTTTCACCCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAATCACTCTCACAAAT
GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
GTCGTCGGACGTGCGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ··SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
ATAGCTACCCTCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGA
TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTTTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCCTCTCACAGTGTCTCGTCCTGTGCTTCCTGTGCTGGATGTGCGA

FIGURE 45 Continuation

601 •SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ••AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 46

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTTGTGGACACCAAGAAGGAAGAGGACCACC

51 · ·AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 ·ValSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnSerProGlyLys
TGTCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGTCCCCAGGGA
ACAGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTGAGGGGTCCCT

201 · ·GlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerProTyrTyr
AGGGACTGGAGTGGATTGGATATATCTATTACAGTGGGAGTCCCTATTAC
TCCTTGACCTCACCTAACCTATATAGATAATGTCACCCTCAGGGATAATG

251 AsnProSerLeuLysSerArgValThrIleSerAlaAspThrSerLysAsn
AACCCTCCCTCAAGAGTCGAGTCACTATATCTGCAGACACGTCCAAGAA
TTGGGGAGGGAGTTCTCAGCTCAGTGATATAGACGTCTGTGCAGGTTCTT

301 ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaIleTyr
CCAATTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCATTT
GGTTAAGAGGGACTTCGACTCGAGACACTGGCGAGGCCTGTGCCGGTAAA

351 · ·TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTTTTGAACCCTAACCTCTGATGACCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

451 ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGCGGGACCCGA

501 · ·LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCA
CGGACCAGTTCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
GGCGCTCTGACCAGCGCGTGCACACCTTCCCAGCTGTCTACAGTCCCTC
CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG

FIGURE 46 Continuation

•GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
601 AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
TCTGAGATGAGGGAGTCGTGCGACCACTGGCACGGGAGGTCGTTGAAGC

••ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
651 GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCCGGTGGTTGTGGTTC

ValAspLysThrVal
701 GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751 TGGAAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
GGTCCGGTCCCGTTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCAC
AGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAAAAGTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCCTACCCAGGCCCTTCACA
GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCC

1001 ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAACTGTCCACTCCCT
TGGGACGGGGACTGGATTCCGGTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
GTGAGCCTGTGGAAGAGAGGAGGTCTAGGCTCATTGAGGGTTAGAAGA

GluArgLysCysCysValGluCysProProCysPro
1101 CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCAGGTAAGC
GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCC

1151 CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
GTCCGGTCCGGAGCGGGAGGTTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
CGGACGTAGGTECCTGTCCGGGGTTCGACCCACGACTGTGCAGGTGGAGGT

AlaProProValAlaGlyProSerValPheLeuPhePro
1251 TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCTCTTCCCC
AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
1301 CCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG

FIGURE 46 Continuation

GGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

1351 ·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

1401 ··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

1451 GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
CAGTTCAACAGCACGTTCGGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
GTCAAGTTGTCTGTGCAAGGCACACAGTCGCAGGAGTGGCAACACGTGGT

1501 ·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
CCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGTTTCCGG

1551 ··ProAlaProIleGluLysThrIleSerLysThrLys
TCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCCTGGGCG

1601 GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGGCCACCCTCTGCCC
CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

1651 GlyGlnProArgGlu
TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

1701 ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

1751 ·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG
CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

1801 ··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
TGGAGTGGGAGAGCAATGGGCAGCCGAGACAACACTACAAGACCACACCT
ACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

1851 ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
CCCATGCTGGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCA

1901 ·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis
GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

FIGURE 46 Continuation

1951 ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
 ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
 TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

2001 GlyLys
 GGTAAA
 CCATTT

FIGURE 47

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACG

51 ••LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTCTGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACAGCCTCTGTCTCAGTGGTAGTGAACGGCCCCG

151 •SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ••AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAAT
GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 •SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCACTTATTACTGTCTACAGCATA
GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ••SerTyrProProThrPheGlyProGlyThrLysValAspIleLysArg
ATAGTTACCCTCCCCTTTTCGGCCCTGGGACCAAGGTGGATATCAAACGA
TATCAATGGGAGGGTGAAAGCCGGGACCCTGGTTCCACCTATAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 •LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ••GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCCGA

FIGURE 47 Continuation

601 ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 48

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGG
TACTTTGTAGACACCAAGAAGGAAGAGGACCACC

51 ••AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCCA
GTCGAGGGTCTA••CAGGACAGGGTCCACGTCGACGTCTCAGCCCCGGT

101 GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACCTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 •GlySerIleSerArgTyrTyrTrpSerTrpIleArgGlnProProGlyLys
TGGCTCCATCAGTCGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGA
ACCGAGGTAGTCAGCAATGATGACCTCGACCTAGGCCGTGGGGGTCCCT

201 ••GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGCACCTACTAC
TCCCTGACCTCACCTAACCATAACAGAGAATGTACCCCTCGTGGATGATG

251 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsn
AACCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAA
TTGGGGAGGGAGTTCTCAGCTCAGTGGTATAGTCATCTGTGCAGGTTCTT

301 •GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGCACA

351 ••TyrCysAlaArgAspLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
ATTACTGTGCGAGAGATAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
TAATGACACGCTCTCTATTTGACCCCTAACCTCTGATGACCCCGGTCCCT

401 ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTCCCCGGTAGCCAGAAGGG

451 •LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGGCGGGACCCGA

501 ••LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCA
CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

551 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
GGCGCTCTGACCAGCGGCGTGACACCTTCCCAGCTGTCTACAGTCCTC
CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG

FIGURE 48 Continuation

601 •GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

651 ••ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG.
CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCTGTTGTGGTTC

701 ValAspLysThrVal
GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCACAGACG

751 TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801 CCAGCCCAGGGCAGCAAGGCAGGCCCATCTGTCTCCTCACCCGGAGGCC
GGTCGGGTCCCGTCCGTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851 TCTGCCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTCCAC
AGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAAGACCGAAAAGSTG

901 CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTTCACA
GTCCGAGGTCCGTCCGTGCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951 CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCC

1001 ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAACTGTCCACTCCCT
TGGGACGGGGACTGGATTCCGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051 CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
GTCGAGCCTGTGGAAGAGAGGAGGTCTAGGCTCATTGAGGGTTAGAAGA

1101 GluArgLysCysCysValGluCysProProCysPro
CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGC
GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCTG

1151 CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
GTCGGGTCCGGAGCGGGAGGTCGAGTTCGCCCTGTCCACGGGATCTCAT

1201 GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

1251 AlaProProValAlaGlyProSerValPheLeuPhePro
TCTCTTCCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys

FIGURE 48 Continuation

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1301  CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
      GGT TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGAC
      ·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
1351  CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
      GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA
      ··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
      TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC
      GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
1451  CAGTTC AACAGCACGTTC CGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
      GTCAAGTTGTCTGTGCAAGGCACACCAAGTTCGCAGGAGTGGCAACACGTGGT
      ·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
1501  GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
      CCTGACCGACTTGCCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTCCGG
      ··ProAlaProIleGluLysThrIleSerLysThrLys
1551  TCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
      AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCTGGGCG
      GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGGCCACCCTCTGCCC
1601  CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG
      GlyGlnProArgGlu
1651  TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
      ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT
      ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
1701  CCACAGGTGTACACCCTGCCCCCATCCGGGAGGAGATGACCAAGAACCA
      GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT
      ·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
1751  GGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCG
      CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC
      ··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801  TGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACACCT
      ACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGTGGA
      ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
1851  CCCATGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGT
      GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCA
      ·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis
1901  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC

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FIGURE 48 Continuation

CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

1951 ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

2001 GlyLys
GGTAAA
CCATTT

FIGURE 49

1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
ATGAGGCTCCCTGCTCAGCTCCTGGGGCTCCTGC
TACTCCGAGGGACGAGTCGAGGACCCCGAGGACG

51 ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

151 ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCGGGGA
TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGCCCT

201 ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
TTCGGGGATTTCGGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
GGTAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
GTCGTCGGACGTGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ··SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
ATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
TATCAATGGGCACGTCAAACCGGTCCCCTGGTTCGACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
GAAATCTGGAAGTGTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

501 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
GAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAAC
CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
AGGGTCCTCTCACAGTGTCTCGTCCTGTCTGCTGCTGGATGTCGGA

FIGURE 49 Continuation

601 •SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ••AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCCAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA

FIGURE 50

1 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
ATGAAGCATCTGTGGTTCTTCCTCCTGCTGGTGG
TACTTCGTAGACACCAAGAAGGAGGACGACCACC.

51 ••AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCCA
GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCCGGT

101 GlyLeuValLysProLeuGlnThrLeuSerLeuThrCysThrValSerGly
GGACTGGTGAAGCCTTTACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
CCTGACCACTTCGGAAATGTCTGGGACAGGGAGTGGACGTGACAGAGACC

151 •GlySerIleSerSerGlyValTyrTyrTrpSerTrpIleArgGlnHisPro
TGGCTCCATCAGCAGTGGTGTCTTACTACTGGAGCTGGATCCGCCAGCACC
ACCGAGGTAGTCGTCACCACAAATGATGACCTCGACCTAGGCGGTCTGTGG

201 ••GlyLysGlyLeuGluTrpIleGlyTyrIleTyrAsnSerLysThrSer
CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAACAGTAAGACCTCC
GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTGTCATTCTGGAGG

251 TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
TATTATAATCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
ATAATATTAGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

301 •LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

351 ••ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
CCGTGTATTACTGTGCGAGAGATAAATTGGGGATCGCGGACTACTGGGGC
GGCACATAATGACACGCTCTCTATTTAACCCCTAGCGCCTGATGACCCCG

401 GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCA

451 •PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCC
GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTGCGCGGG

501 ••GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGG
ACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

551 AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
AACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCTTACA
TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT

FIGURE 50 Continuation

601 ·SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
GTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
CAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGT

651 ··PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
ACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC
TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCTGTTG

701 ThrLysValAspLysThrVal
ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
TGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751 GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCGTGGACGCACCCCGGCTGT
CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801 GCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCG
CGTCGGGGTCCGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGC

851 GAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
CTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAAGACCGAAA

901 TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCCAGGCCC
AAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951 TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
AAGTGTGTGTCCCGTCCACGAACCGAGTCTGGACGGTTTTTCGGTATAGG

1001 GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
CCCTCCTGGGACGGGGACTGGATTCCGGCTGGGGTTTCCGGTTTGACAGGT

1051 CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

1101 GluArgLysCysCysValGluCysProProCysPro
TCTTCTCTCTGCAGAGCGCAAATGTTGTGTGCGAGTGCCACCGTGCCAG
AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTC

1151 GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
CATTCCGGTCGGGTCCGGAGCGGGAGGTCGAGTCCGCCCTGTCCACGGGA

1201 AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

1251 AlaProProValAlaGlyProSerValPheLeu
CCTCCATCTCTTCTCAGCACCACTGTGGCAGGACCGTCAGTCTTCTCTC
GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal

FIGURE 50 Continuation

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1301  TTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
      AAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

      ·ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
1351  CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA
      GTGCACGCACCACCACCTGCACTCGGTGCTTCTGGGGGTCCAGGTCAAGT

      ··TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
1401  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
      TGACCATGCACCTGCCGGACCTCCACGTATTACGGTTCTGTTTCGGTGCC

      GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
1451  GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACC GTTGT
      CTCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

      ·HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
1501  GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
      CGTGGTCCTGACCGACTTGCCGTTCTCATGTTACGTTCCAGAGGTTGT

      ··GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
1551  AAGGCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
      TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTGGTTTCCACCC

1601  ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCT
      TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

      GlyGlnPro
1651  CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
      GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCTGGG

      ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
1701  CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAA
      GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTT

      ·AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
1751  GAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACA
      CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCTGCTGT

      ··AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
1801  TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACA ACTACAAGACC
      AGCGGCACCTCACCTCTCGTTACCCGTGGGCCTCTTGTTGATGTTCTGG

      ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
1851  ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCT
      TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCTGA

      ·ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
1901  CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG

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FIGURE 50 Continuation

GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

• •MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu

1951 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG

ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

SerProGlyLys

2001 TCTCCGGGTAAA

AGAGGCCCATTT

FIGURE 51

1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
 ATGAGGGTCCCTGCTCAGCTCCTGGGGCTCCTGC
 TACTCCCAGGGACGAGTCGAGGACCCCGAGGACG

51 ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
 TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
 ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

101 SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgThr
 TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGAC
 AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCTG

151 ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
 AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
 TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

201 ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
 AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
 TTCGGGGATTTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCAG

251 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAAT
 GGTAGTTCCAAGTCGCCGTACCTAGACCCTGTCTTAAGTGAGAGTGTTA

301 ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
 CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
 GTCGTCGGACGTCCGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

351 ··SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
 ATAGCTACCCTCCCCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
 TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTCTAGTTTGCT

401 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
 ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
 TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

451 ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
 GAAATCTGGAAGTCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
 CTTTAGACCTTGACGATCGCAACACGACGACTTATTGAAGATAGGGT

501 ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
 GAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAAC
 CTCTCCGGTTTCATGTACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

551 SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
 TCCAGAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
 AGGGTCCCTCTCAGTGTCTCGTCCTGTCGTTCCCTGTCGTGGATGTCGGA

FIGURE 51 Continuation

601 •SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
CAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

651 ••AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
ACGCCTGCCAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

701 PheAsnArgGlyGluCys
TTCAACAGGGGAGAGTGT
AAGTTGTCCCCTCTCACA